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Om protein - protein search, using sw model

Run on: April 8, 2003, 14:31:47 ; Search time 93 Seconds
 (without alignments)
 1207.480 Million cell updates/sec

Title: US-09-001-737-8

Perfect score: 545

Sequence: I MAKEIKFSNDARAAAMVRGVDD.....TPAPAMPAGMDPQMMGSGMGG 545

Scoring table: OLIGO

searched: 671580 seqs., 205047115 residues

Word size : 8

Total number of hits satisfying chosen parameters: 564

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL 211:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_micr:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_uniclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaip:*
- 17: sp_archeip:*

Pre-d. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
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| 2 | 184 | 33.8 | 184 | 2 | 09L6F1 |
| 3 | 156 | 28.6 | 159 | 2 | 08RJH4 |
| 4 | 141 | 25.9 | 184 | 2 | 093TK8 |
| 5 | 100 | 18.3 | 159 | 2 | 08RJ42 |
| 6 | 91 | 16.7 | 184 | 2 | 093TK4 |
| 7 | 86 | 15.8 | 184 | 2 | 093TL2 |
| 8 | 80 | 14.7 | 184 | 2 | 093TK9 |
| 9 | 80 | 14.7 | 184 | 2 | 093TK7 |
| 10 | 78 | 14.3 | 184 | 2 | 08RJ02 |
| 11 | 78 | 14.3 | 184 | 2 | 093TK3 |
| 12 | 78 | 14.3 | 184 | 2 | 09AM57 |
| 13 | 78 | 14.3 | 184 | 2 | 069135 |
| 14 | 75 | 13.8 | 184 | 2 | 09X455 |
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17 67 12.3 540 2 Q8Vt58 streptococcus
 18 58 10.6 541 2 Q93E66 enteroococcus
 19 56 10.3 542 2 Q9ArP7 lactobacillus
 20 55 10.1 543 2 Q9KU23 lactobacillus
 21 47 8.6 184 2 Q93T13 streptococcus
 22 43 7.9 184 2 Q93T5 streptococcus
 23 36 6.6 184 2 Q9L6F4 streptococcus
 24 36 6.6 184 2 Q916F0 streptococcus
 25 36 6.6 184 2 Q916F7 streptococcus
 26 36 6.6 184 2 Q9L6F6 streptococcus
 27 36 6.6 184 2 Q916F3 streptococcus
 28 36 6.6 184 2 Q93T11 streptococcus
 29 36 6.6 184 2 Q93T10 streptococcus
 30 34 6.2 184 2 Q9L6F5 streptococcus
 31 34 6.2 184 2 Q9K1S5 streptococcus
 32 34 6.2 184 2 Q9K56 streptococcus
 33 34 6.2 184 2 Q916F9 streptococcus
 34 34 6.2 184 2 Q916F8 streptococcus
 35 34 6.2 184 2 Q9L6F8 streptococcus
 36 33 6.1 184 2 Q9K1S5 streptococcus
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 39 32 5.9 184 2 Q9K1S0 streptococcus
 40 32 5.9 184 2 Q916F2 streptococcus
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 68 29 5.3 184 2 Q9FFB3 streptococcus
 69 28 5.1 184 2 Q9FFB9 streptococcus
 70 28 5.1 184 2 Q9FFB6 streptococcus
 71 28 5.1 184 2 Q9RFB0 streptococcus
 72 27 5.0 184 2 Q9XCA9 streptococcus
 73 26 4.8 184 2 Q916F7 streptococcus
 74 26 4.8 184 2 Q93Gv8 streptococcus
 75 26 4.8 184 2 Q93Gv8 streptococcus
 76 26 4.8 184 2 Q9VtM8 streptococcus
 77 26 4.8 184 2 Q9VtM6 streptococcus
 78 26 4.8 184 2 Q9SSL7 streptococcus
 79 26 4.8 184 2 Q9KkF0 clostridium
 80 25 4.6 184 2 Q9KjV7 clostridium
 81 25 4.6 184 2 Q8Vv4 bacillus th
 82 25 4.6 184 2 Q9rc20 bacillus sp
 83 25 4.6 184 2 Q9zv4 bacillus st
 84 25 4.6 184 2 Q98119 rhizobium l
 85 24 4.4 184 2 Q9Vq27 campylobacter
 86 24 4.4 184 2 Q8Vr20 chlamydophili
 87 24 4.4 184 2 Q8Vq28 campylobacter
 88 24 4.4 184 2 Q9X4G5 chlamydophili
 89 24 4.4 184 2 Q956B0 chlamydophili

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| 99 | 23 | 4.2 | 553 | 2 | 09REU4 |
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| 111 | 22 | 4.0 | 563 | 2 | 093FPX4 |
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| 238 | 15 | 2.8 | 581 | 5 | Q96219 | 096219 culicoides | 0911ub toxoplasma |
| 239 | 15 | 2.8 | 582 | 5 | Q90517 | 090517 paracentrot | 0911ub toxoplasma |
| 240 | 15 | 2.8 | 598 | 5 | Q9XW7 | 09XW7 onchocerca | 0911ub toxoplasma |
| 241 | 15 | 2.6 | 82 | 2 | Q9F4F3 | 09F4f3 buchnera ap | 0911je4 arribidopsis |
| 242 | 14 | 2.6 | 82 | 2 | Q9F4F1 | 09F4f1 buchnera ap | p33570 solanum tub |
| 243 | 14 | 2.6 | 82 | 2 | Q9F4E9 | 09F4e9 buchnera ap | 09av2 arabidopsis |
| 244 | 14 | 2.6 | 82 | 2 | Q9F4E7 | 09F4e7 buchnera ap | 091wt6 oriza sativ |
| 245 | 14 | 2.6 | 82 | 2 | Q9F4E5 | 09F4e5 buchnera ap | 095y66 tetrathyrema |
| 246 | 14 | 2.6 | 82 | 2 | Q9F4E3 | 09F4e3 buchnera ap | 09x2u0 staphyloc |
| 247 | 14 | 2.6 | 191 | 2 | Q9VU52 | 09VU52 | 093a38 leptospira |
| 248 | 14 | 2.6 | 574 | 3 | Q9P521 | 09P521 neurospora | 08vvcs5 anaerobiosp |
| 249 | 14 | 2.6 | 594 | 3 | Q9A10 | 09A10 desulfobacto | 093m74 analasma p |
| 250 | 14 | 2.6 | 550 | 2 | Q9S303 | 09S303 rickettsia | 08vsa8 wolbachia e |
| 251 | 14 | 2.6 | 550 | 2 | Q9VQ17 | 09VQ17 rickettsia | 093nn2 analasma p |
| 252 | 14 | 2.6 | 555 | 2 | Q9x603 | 09x603 primary end | 0933c9 analasma p |
| 253 | 14 | 2.6 | 572 | 10 | Q9R1W0 | 09R1w0 arribidopsis | 0913k9 analasma p |
| 254 | 14 | 2.6 | 574 | 3 | Q9P521 | 09P521 neurospora | 094kmg analasma m |
| 255 | 14 | 2.6 | 594 | 3 | Q9A10 | 09A10 coccidiode | 091cc62 ehrlichia s |
| 256 | 13 | 2.4 | 174 | 10 | P93571 | 093571 solanum tub | 091c61 ehrlichia s |
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| 258 | 13 | 2.4 | 183 | 2 | Q9VU14 | 09VU14 bacillus th | 093j73 ehrlichia m |
| 259 | 13 | 2.4 | 184 | 2 | Q9347 | 09347 bacillus th | 093l13 desulfobacto |
| 260 | 13 | 2.4 | 184 | 2 | Q9346 | 09346 bacillus an | 093ld1 analasma p |
| 261 | 13 | 2.4 | 184 | 2 | Q93R45 | 093r45 bacillus ce | 093l22 analasma p |
| 262 | 13 | 2.4 | 184 | 2 | Q93QK6 | 093QK6 vibrrio chol | 093m5 vibr analasma p |
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| 265 | 13 | 2.4 | 184 | 2 | Q9681 | 09681 yersinia en | 09rwg9 desinococcus |
| 266 | 13 | 2.4 | 184 | 2 | Q9VU16 | 09VU16 bacillus an | 0981t3 onchocerca |
| 267 | 13 | 2.4 | 184 | 2 | Q9VU15 | 09VU15 bacillus ce | 000334 wolbachia s |
| 268 | 13 | 2.4 | 185 | 2 | Q93QK8 | 093QK8 vibrrio harv | 091981 guillardia |
| 269 | 13 | 2.4 | 185 | 2 | Q93QK7 | 093QK7 vibrrio chol | 09aw03 guillardia |
| 270 | 13 | 2.4 | 185 | 2 | Q93QK4 | 093QK4 vibrrio cinc | 00373 analasma p |
| 271 | 13 | 2.4 | 185 | 2 | Q93QK3 | 093QK3 photobacter | 093an7 mycobacteri |
| 272 | 13 | 2.4 | 185 | 2 | Q93QK0 | 093QK1 vibrrio fluv | 093en6 mycobacteri |
| 273 | 13 | 2.4 | 185 | 2 | Q93QJ4 | 093QK0 vibrrio fluv | 093en5 mycobacteri |
| 274 | 13 | 2.4 | 185 | 2 | Q93QJ9 | 093QJ9 vibrrio para | 093l02 pseudosuga |
| 275 | 13 | 2.4 | 185 | 2 | Q93QJ8 | 093QJ8 vibrrio para | 094021 pseudosuga |
| 276 | 13 | 2.4 | 185 | 2 | Q93QJ7 | 093QJ7 vibrrio para | 094021 pseudosuga |
| 277 | 13 | 2.4 | 185 | 2 | Q93QJ6 | 093QJ6 vibrrio mimi | 091672 mycobacteri |
| 278 | 13 | 2.4 | 185 | 2 | Q93QJ5 | 093QJ5 vibrrio orda | 091671 mycobacteri |
| 279 | 13 | 2.4 | 185 | 2 | Q93QJ4 | 093QJ4 vibrrio para | 091670 mycobacteri |
| 280 | 13 | 2.4 | 185 | 2 | Q93QJ3 | 093QJ3 vibrrio para | 091666 mycobacteri |
| 281 | 13 | 2.4 | 185 | 2 | Q93QJ2 | 093QJ2 vibrrio para | 091662 mycobacteri |
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| 284 | 13 | 2.4 | 185 | 2 | Q93QI8 | 093QI8 aeromonas h | 091667 mycobacteri |
| 285 | 13 | 2.4 | 185 | 2 | Q93QI7 | 093QI7 plesiomonas | P2164 pseudomonas |
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| 295 | 13 | 2.4 | 185 | 2 | Q93QI1 | 093QI1 yersinia angu | 093q93 mycobacteri |
| 296 | 13 | 2.4 | 185 | 2 | Q93QI0 | 093QI0 vibrrio chol | 093q94 mycobacteri |
| 297 | 13 | 2.4 | 185 | 2 | Q93QI21 | 093QI21 vibrrio alg | 093q95 mycobacteri |
| 298 | 13 | 2.4 | 185 | 2 | Q93QI29 | 093QI29 vibrilo vuln | 093q96 mycobacteri |
| 299 | 13 | 2.4 | 186 | 2 | Q93QI24 | 093QI24 shigella so | 093q97 mycobacteri |
| 300 | 13 | 2.4 | 186 | 2 | Q93QI23 | 093QI23 prevotella | 093q98 mycobacteri |
| 301 | 13 | 2.4 | 186 | 2 | Q93QI22 | 093QI22 prevotella | 093q99 mycobacteri |
| 302 | 13 | 2.4 | 186 | 2 | Q93QI21 | 093QI21 vibrilo angu | 093q90 mycobacteri |
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| 305 | 13 | 2.4 | 186 | 2 | Q93QI18 | 093QI18 prevotella | 093q93 mycobacteri |
| 306 | 13 | 2.4 | 186 | 2 | Q93QI17 | 093QI17 vibrilo vuln | 093q94 mycobacteri |
| 307 | 13 | 2.4 | 186 | 2 | Q93QI16 | 093QI16 prevotella | 093q95 mycobacteri |
| 308 | 13 | 2.4 | 186 | 2 | Q93QI15 | 093QI15 vibrilo vuln | 093q96 mycobacteri |
| 309 | 13 | 2.4 | 186 | 2 | Q93QI14 | 093QI14 vibrilo vuln | 093q97 mycobacteri |
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| 319 | 13 | 2.4 | 186 | 2 | Q93QI04 | 093QI04 vibrilo vuln | 093qa7 mycobacteri |
| 320 | 13 | 2.4 | 186 | 2 | Q93QI03 | 093QI03 vibrilo vuln | 093qa8 mycobacteri |
| 321 | 13 | 2.4 | 186 | 2 | Q93QI02 | 093QI02 vibrilo vuln | 093qa9 mycobacteri |
| 322 | 13 | 2.4 | 186 | 2 | Q93QI01 | 093QI01 vibrilo vuln | 093qa10 mycobacteri |
| 323 | 12 | 2.2 | 410 | 2 | Q9RM17 | 09RM17 vibrilo vuln | 093qa11 mycobacteri |
| 324 | 12 | 2.2 | 548 | 16 | Q9RW09 | 09RW09 vibrilo vuln | 093qa12 mycobacteri |
| 325 | 12 | 2.2 | 523 | 2 | Q9RT33 | 09RT33 vibrilo vuln | 093qa13 mycobacteri |
| 326 | 12 | 2.2 | 526 | 2 | Q93ID1 | 093ID1 vibrilo vuln | 093qa14 mycobacteri |
| 327 | 12 | 2.2 | 405 | 2 | Q9XB99 | 09XB99 vibrilo vuln | 093qa15 mycobacteri |
| 328 | 12 | 2.2 | 409 | 2 | Q9LC62 | 09LC62 vibrilo vuln | 093qa16 mycobacteri |
| 329 | 12 | 2.2 | 410 | 2 | Q9RM12 | 09RM12 vibrilo vuln | 093qa17 mycobacteri |
| 330 | 12 | 2.2 | 548 | 16 | Q9RW09 | 09RW09 vibrilo vuln | 093qa18 mycobacteri |
| 331 | 12 | 2.2 | 523 | 2 | Q9RT33 | 09RT33 vibrilo vuln | 093qa19 mycobacteri |
| 332 | 12 | 2.2 | 526 | 2 | Q93ID1 | 093ID1 vibrilo vuln | 093qa20 mycobacteri |
| 333 | 12 | 2.2 | 405 | 2 | Q9XB99 | 09XB99 vibrilo vuln | 093qa21 mycobacteri |
| 334 | 12 | 2.2 | 409 | 2 | Q9LC62 | 09LC62 vibrilo vuln | 093qa22 mycobacteri |
| 335 | 12 | 2.2 | 410 | 2 | Q9RM12 | 09RM12 vibrilo vuln | 093qa23 mycobacteri |
| 336 | 12 | 2.2 | 541 | 2 | Q9RT33 | 09RT33 vibrilo vuln | 093qa24 mycobacteri |
| 337 | 12 | 2.2 | 523 | 2 | Q9RT33 | 09RT33 vibrilo vuln | 093qa25 mycobacteri |
| 338 | 12 | 2.2 | 526 | 2 | Q93ID1 | 093ID1 vibrilo vuln | 093qa26 mycobacteri |
| 339 | 12 | 2.2 | 405 | 2 | Q9XB99 | 09XB99 vibrilo vuln | 093qa27 mycobacteri |
| 340 | 12 | 2.2 | 409 | 2 | Q9LC62 | 09LC62 vibrilo vuln | 093qa28 mycobacteri |
| 341 | 12 | 2.2 | 410 | 2 | Q9RM12 | 09RM12 vibrilo vuln | 093qa29 mycobacteri |
| 342 | 12 | 2.2 | 541 | 2 | Q9RT33 | 09RT33 vibrilo vuln | 093qa30 mycobacteri |
| 343 | 11 | 2.0 | 98 | 2 | Q9L672 | 09L672 vibrilo vuln | 093qa31 mycobacteri |
| 344 | 11 | 2.0 | 84 | 2 | Q93EN6 | 093en6 vibrilo vuln | 093qa32 mycobacteri |
| 345 | 11 | 2.0 | 84 | 2 | Q93EN5 | 093en5 vibrilo vuln | 093qa33 mycobacteri |
| 346 | 11 | 2.0 | 84 | 2 | Q93EN4 | 093en4 vibrilo vuln | 093qa34 mycobacteri |
| 347 | 11 | 2.0 | 98 | 2 | Q9L671 | 09L671 vibrilo vuln | 093qa35 mycobacteri |
| 348 | 11 | 2.0 | 98 | 2 | Q91666 | 091666 vibrilo vuln | 093qa36 mycobacteri |
| 349 | 11 | 2.0 | 98 | 2 | Q91667 | 091667 vibrilo vuln | 093qa37 mycobacteri |
| 350 | 11 | 2.0 | 99 | 2 | Q91667 | 091667 vibrilo vuln | 093qa38 mycobacteri |
| 351 | 11 | 2.0 | 98 | 2 | Q91670 | 091670 vibrilo vuln | 093qa39 mycobacteri |
| 352 | 11 | 2.0 | 98 | 2 | Q91666 | 091666 vibrilo vuln | 093qa40 mycobacteri |
| 353 | 11 | 2.0 | 98 | 2 | Q91666 | 091666 vibrilo vuln | 093qa41 mycobacteri |
| 354 | 11 | 2.0 | 98 | 2 | Q91666 | 091666 vibrilo vuln | 093qa42 mycobacteri |
| 355 | 11 | 2.0 | 98 | 2 | Q91666 | 091666 vibrilo vuln | 093qa43 mycobacteri |
| 356 | 11 | 2.0 | 99 | 2 | Q91667 | 091667 vibrilo vuln | 093qa44 mycobacteri |
| 357 | 11 | 2.0 | 107 | 2 | P72164 | 092164 pseudomonas | 093qa45 mycobacteri |
| 358 | 11 | 2.0 | 107 | 2 | P75021 | 095021 pseudomonas | 093qa46 mycobacteri |
| 359 | 11 | 2.0 | 107 | 2 | P75021 | 095021 pseudomonas | 093qa47 mycobacteri |
| 360 | 11 | 2.0 | 107 | 2 | P75021 | 095021 pseudomonas | 093qa48 mycobacteri |
| 361 | 11 | 2.0 | 113 | 2 | Q98672 | 098672 chlamydia p | 093qa49 mycobacteri |
| 362 | 11 | 2.0 | 114 | 2 | Q95X55 | 095x55 mycobacteri | 093qa50 mycobacteri |
| 363 | 11 | 2.0 | 114 | 2 | Q95X44 | 095x44 mycobacteri | 093qa51 mycobacteri |
| 364 | 11 | 2.0 | 114 | 2 | Q93QAL | 093qal mycobacteri | 093qa52 mycobacteri |
| 365 | 11 | 2.0 | 114 | 2 | Q93QAO | 093qa0 mycobacteri | 093qa53 mycobacteri |
| 366 | 11 | 2.0 | 114 | 2 | Q93Q99 | 093q99 mycobacteri | 093qa54 mycobacteri |
| 367 | 11 | 2.0 | 114 | 2 | Q93Q90 | 093q90 mycobacteri | 093qa55 mycobacteri |
| 368 | 11 | 2.0 | 114 | 2 | Q93Q94 | 093q94 mycobacteri | 093qa56 mycobacteri |
| 369 | 11 | 2.0 | 114 | 2 | Q93Q92 | 093q92 mycobacteri | 093qa57 mycobacteri |
| 370 | 11 | 2.0 | 120 | 2 | Q96321 | 096321 mycobacteri | 093qa58 mycobacteri |
| 371 | 1 | | | | | | |

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|-----|---|-----|------|----|--------|---------------------|--|
| 528 | 9 | 1.7 | 580 | 5 | 096783 | 096783 plectus acu | DR PROSITE; PS00296; CHAPERONINS_CPN60; 1. |
| 529 | 8 | 1.5 | 44 | 5 | 09T273 | 09t273 brassica na | KW Atp-binding; Chaperone. |
| 530 | 8 | 1.5 | 98 | 2 | 09L662 | 09pdg1 mycopacteri | FT NON_TER |
| 531 | 8 | 1.5 | 131 | 16 | 09PDG1 | 09pdg1 xylella fas | SQ 1 |
| 532 | 8 | 1.5 | 146 | 17 | 08PT81 | P7081 methanobarc | Query Match 55.8%; Score 304; DB 2; Length 100.0%; Pred. No. 2.4e-304; Mismatches 0; Ind |
| 533 | 8 | 1.5 | 156 | 2 | P7081 | P7081 agrobacteri | Best Local Similarity 100.0%; Pred. No. 2.4e-304; Mismatches 0; Ind |
| 534 | 8 | 1.5 | 161 | 9 | 094121 | 094mz1 haemophilus | Matches 304; Conservative 0; Mismatches 0; Ind |
| 535 | 8 | 1.5 | 180 | 2 | 09KB9 | 09kb9 leifsonia a | DR |
| 536 | 8 | 1.5 | 184 | 2 | 09S337 | 09s337 staphylococ | DR |
| 537 | 8 | 1.5 | 184 | 2 | 09X01 | 09x01 staphylococ | DR |
| 538 | 8 | 1.5 | 191 | 16 | 09R53 | 09r53 neisseria m | DR |
| 539 | 8 | 1.5 | 197 | 16 | 09N02 | 09n02 rhizobium l | DR |
| 540 | 8 | 1.5 | 235 | 16 | 09K61 | 0926f1 rhizobium m | DR |
| 541 | 8 | 1.5 | 326 | 10 | 09X05 | 09x15 avicennia m | DR |
| 542 | 8 | 1.5 | 333 | 16 | 080659 | 080659 agrobacteri | DR |
| 543 | 8 | 1.5 | 343 | 16 | 09H08 | 097pd8 staphylococ | DR |
| 544 | 8 | 1.5 | 366 | 5 | 02B330 | 02B330 entamoeba h | DR |
| 545 | 8 | 1.5 | 391 | 2 | 09R4C5 | 09rmc5 acetobacter | DR |
| 546 | 8 | 1.5 | 429 | 10 | 092M7 | 093zm7 arribidopsis | DR |
| 547 | 8 | 1.5 | 431 | 2 | 052146 | 05146 mycobacter | DR |
| 548 | 8 | 1.5 | 440 | 10 | 094CF5 | 094cf5 arribidopsis | DR |
| 549 | 8 | 1.5 | 473 | 3 | 09H08 | 09ifq8 emericella | DR |
| 550 | 8 | 1.5 | 524 | 10 | 09JX1 | 09jx1 arabidopsis | DR |
| 551 | 8 | 1.5 | 535 | 5 | 015782 | 015782 entamoeba h | DR |
| 552 | 8 | 1.5 | 538 | 2 | 0934A4 | 0934a4 actinobacil | DR |
| 553 | 8 | 1.5 | 544 | 17 | 09BE9 | 097be9 thermoplasma | DR |
| 554 | 8 | 1.5 | 549 | 17 | 02ZVU7 | 08zvu7 pyrococcus | DR |
| 555 | 8 | 1.5 | 549 | 17 | 09n216 | 08zt16 pyrococcus | DR |
| 556 | 8 | 1.5 | 592 | 4 | 09RD2 | 09i0d2 homo sapien | DR |
| 557 | 8 | 1.5 | 851 | 10 | 023524 | 023524 arribidopsis | DR |
| 558 | 8 | 1.5 | 1113 | 4 | 09N94 | 086n94 homo sapien | DR |
| 559 | 8 | 1.5 | 1249 | 5 | 09TV1 | 095tv1 drosophila | DR |
| 560 | 8 | 1.5 | 1278 | 4 | 08WR4 | 08wr4 homo sapien | DR |
| 561 | 8 | 1.5 | 1325 | 10 | 084533 | 064533 arribidopsis | DR |
| 562 | 8 | 1.5 | 1371 | 16 | 08X042 | 08x042 arribidopsis | DR |
| 563 | 8 | 1.5 | 1504 | 5 | 09TV86 | 09tv86 drosophila | DR |
| 564 | 8 | 1.5 | 1975 | 5 | 09Vcd1 | 09vcd1 drosophila | DR |

ALIGNMENTS

| | | | | | | | |
|----------|--|--|------|---------|--|--|--|
| RESULT 1 | | | | | | | |
| 033733 | | PRELIMINARY; | PRC; | 481 AA. | | | |
| ID | 033733 | (TREMBREL; 05, Created) | | | | | |
| AC | 033733; | (TREMBREL; 05, Last sequence update) | | | | | |
| DT | 01-JAN-1998 | (TREMBREL; 05, Last annotation update) | | | | | |
| DT | 01-JAN-1998 | (TREMBREL; 05, Last annotation update) | | | | | |
| DT | 01-MAR-2002 | (TREMBREL; 20, Last annotation update) | | | | | |
| DE | 60 | KDa chaperonin (Protein Cpn60) (Fragment). | | | | | |
| GN | GROEL. | | | | | | |
| OS | Streptococcus pyogenes. | | | | | | |
| OC | Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococciaceae; Streptococcus. | | | | | | |
| OX | NCBI_TAXID=114; | | | | | | |
| RN | [1] | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
| RL | Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. | | | | | | |
| CC | -I- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY). | | | | | | |
| CC | -I- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY). | | | | | | |
| CC | -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY. | | | | | | |
| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
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| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
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| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
| RL | Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. | | | | | | |
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| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
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| CC | -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY. | | | | | | |
| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
| RL | Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. | | | | | | |
| CC | -I- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY). | | | | | | |
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| CC | -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY. | | | | | | |
| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
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| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
| RL | Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. | | | | | | |
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| CC | EMBL: X89236; CAB1520.1; - | | | | | | |
| DR | HSSP: P01339; IGRU. | | | | | | |
| DR | InterPro: IPR0144; Chaperon-Cpn60. | | | | | | |
| DR | PFAM: PF0018; Cpn60_TCF1; I. | | | | | | |
| DR | PRINTS: PRO0398; CHAPERONIN60. | | | | | | |
| DR | PRINTS: PRO0304; TCOMPLEXTCPI. | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | |
| RC | STRAIN=SROTYP M49; | | | | | | |
| P | Pohl, B., Podbielski, A., Zarges, I.; | | | | | | |
| RL | Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases. | | | | | | |
| CC | -I- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY). | | | | | | |
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| CC | -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.</ | | | | | | |

OC Bacteria; Firmicutes; *Bacillus/Clostridium group*; Lactobacillales;
 OC Streptococcaceae; *Streptococcus*.
 OC NCBI_TAXID=1329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC43496;
 RA Goh S.H., Hill J.E., Hemmingsen S.M.;
 RT "Streptococcus species characterized by cpn60 sequence.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF312804; AAK48555_1;
 DR InterPro: IPR002433; Cpn60/TCP-1.
 PRam: PF00118; cpn60_TCPI; 1.
 DR ATP-binding; Chaperone.
 FT NON_TER 184 AA; 184
 FT SEQUENCE 184 AA; 184 AA; 19768 MW; 479C981163B1166E CRC64;
 SQ 25.9%; score 141; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-136; Indels 0; Gaps 0;
 Matches 141; Conservative 0; Mismatches 0;
 RESULT 3
 ORRJH4 PRELIMINARY; PRT: 159 AA.
 ID OBRJH4
 AC OBRJH4
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE 60 kDa chaperonin Cpn60 (Fragment).
 GN CPN60
 OS Streptococcus dysgalactiae.
 OC Bacteroides; Flavimicrobium; *Bacillus/Clostridium group*; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OC NCBI_TAXID=1334;
 RN [1]
 RR SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27957, ATCC 43078, 62, AND 74;
 RA McDonald W.L., Deighton M.A., Fry B.N.;
 RT "Phylogeny comparison of *Streptococcus* sp. associated with bovine
 mastitis using 16S rRNA and newly sequenced HSP60 genes.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF485794; AAL96573_1;
 DR EMBL: AF485795; AAL96574_1;
 DR EMBL: AF485796; AAL96575_1;
 DR EMBL: AF485797; AAL96576_1;
 DR NON_TER 159
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 17216 MW; 079B14AF907433BE CRC64;

Query Match 28.6%; Score 156; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 4.e-152; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 EGKVNVTAGANPPIGIRGRIETATATEVAELKAIAQPVSGKEIAQVAVSSRSEKVEYI 160
 4 EGKVNVTAGANPPIGIRGRIETATATEVAELKAIAQPVSGKEIAQVAVSSRSEKVEYI 63
 QY 161 SEMERYGNDGVITTEESGRMGTELEVEVGMOFRGILSYQMVNDNEKMDENPFILEI 220
 Db 64 SEMERYGNDGVITTEESGRMGTELEVEVGMOFRGILSYQMVNDNEKMDENPFILEI 123
 QY 221 TDKVSNIQDILPYLEEVLTNRPLLIADWDGEA 256
 Db 124 TDKVSNIQDILPYLEEVLTNRPLLIADWDGEA 159

RESULT 4
 O93TK8 PRELIMINARY; PRT: 184 AA.
 ID O93TK8
 AC O93TK8
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE Cpn60 (Fragment).
 GN CPN60.
 OS Streptococcus canis.

OC Bacteria; Firmicutes; *Bacillus/Clostridium group*; Lactobacillales;
 OC Streptococcaceae; *Streptococcus*.
 OC NCBI_TAXID=1329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC43496;
 RA Goh S.H., Hill J.E., Hemmingsen S.M.;
 RT "Streptococcus species characterized by cpn60 sequence.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF312804; AAK48555_1;
 DR InterPro: IPR002433; Cpn60/TCP-1.
 PRam: PF00118; cpn60_TCPI; 1.
 DR ATP-binding; Chaperone.
 FT NON_TER 184 AA; 184
 FT SEQUENCE 184 AA; 184 AA; 19768 MW; 479C981163B1166E CRC64;
 SQ 25.9%; score 141; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-136; Indels 0; Gaps 0;
 Matches 141; Conservative 0; Mismatches 0;
 RESULT 5
 OBRJ42 PRELIMINARY; PRT: 159 AA.
 ID OBRJ42
 AC OBRJ42
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE 60 kDa chaperonin Cpn60 (Fragment).
 GN CPN60.
 OS Streptococcus uberis.
 OC Bacteroides; Flavimicrobium; *Bacillus/Clostridium group*; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OC NCBI_TAXID=1349;
 RN [1]
 RR SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13387, ATCC 700407, 16, AND 33;
 RA McDonald W.L., Deighton M.A., Fry B.N.;
 RT "Phylogeny comparison of *Streptococcus* sp. associated with bovine
 mastitis using 16S rRNA and newly sequenced HSP60 genes.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF485801; AAL96580_1;
 DR EMBL: AF485802; AAL96581_1;
 DR EMBL: AF485803; AAL96582_1;
 DR EMBL: AF485804; AAL96583_1;
 DR NON_TER 159
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 17275 MW; 9C456169FECC22AF CRC64;

Query Match 18.3%; Score 100; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 2.4e-94; Indels 0; Gaps 0;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LKAIQPVSGKEIAQVAVSSRSEKVEYISEMERYGNDGVITTEESGRMGTELEVE 189
 Db 33 LKAIQPVSGKEIAQVAVSSRSEKVEYISEMERYGNDGVITTEESGRMGTELEVE 92
 QY 190 GMQFDRLGILSYQMVNDNEKMDENPFILETDKKVSNIQ 229
 Db 93 GMQFDRLGILSYQMVNDNEKMDENPFILETDKKVSNIQ 132

W d Apr 16 08:08:21 2003

RESULT 6

| | | |
|---|--------------|--------------|
| ID Q8RJG8 | PRELIMINARY: | PRT: 159 AA. |
| AC Q8RJG8; | | |
| DT 01-JUN-2002 (TREMBLrel. 21, Created) | | |
| DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update) | | |
| DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | |
| DE 60 kDa chaperonin Cpn60 (Fragment). | | |
| GN Cpn60 | | |
| SQ STREPTOCOCCUS PARABURS. | | |
| OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; | | |
| OC Streptococcaceae; Streptococcus. | | |
| OX NCBI_TAXID=1348; | | |
| RP [1] SEQUENCE FROM N.A. | | |
| RC STRAIN=ATCC 1386, 21B, AND 25; | | |
| RA McDonald W.L., Deighton M.A., FY B.N.; | | |
| RT "Phylogeny comparison of Streptococcus sp. associated with bovine mastitis using 16S rRNA and newly sequenced Hsp60 genes."; | | |
| RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. | | |
| DR EMBL; AF051798; AAL96577.1; -. | | |
| DR EMBL; AF485799; AAL96578.1; -. | | |
| DR EMBL; AF485800; AAL96579.1; -. | | |
| FT NON-TER 1 1 | | |
| SQ SEQUENCE 159 AA; 17113 MW; 110352BF8F70EFPAD CRC64; | | |
| Query Match Best Local Similarity 100.0%; Pred. No. 4.e-85; Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| OY 139 GKEAIAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 198 | | |
| Db 42 GKEAIAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 101 | | |
| RESULT 7 | | |
| Q93TK4 PRELIMINARY: PRT: 184 AA. | | |
| ID Q93TK4 | | |
| AC 093TK4; | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Created) | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | |
| DE Cpn60 (Fragment). | | |
| GN Cpn60. | | |
| SQ STREPTOCOCCUS PORCINUS. | | |
| OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; | | |
| OC Streptococcaceae; Streptococcus. | | |
| OX NCBI_TAXID=1340; | | |
| RP [1] SEQUENCE FROM N.A. | | |
| RC STRAIN=ATCC43138; | | |
| RA Goh S.H., Hill J.E., Hemmingsen S.M.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | | |
| DR EMBL; AF32810; AAK48861.1; -. | | |
| DR Interpro; IPR002423; Cpn60/TCP-1. | | |
| DR Pfam; PF00118; cpn60_TCP1; 1. | | |
| KW Amp-binding; Chaperone. | | |
| FT NON-TER 1 1 | | |
| SQ SEQUENCE 184 AA; 19848 MW; ECG6BD9A5FAP745A CRC64; | | |
| Query Match Best Local Similarity 100.0%; Pred. No. 1.2e-73; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| OY 140 KEATAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 199 | | |
| Db 50 KEATAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 109 | | |
| RESULT 8 | | |
| Q93TK9 PRELIMINARY: PRT: 184 AA. | | |
| ID Q93TK9 | | |
| AC 093TK9; | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Created) | | |
| DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | |
| DE Cpn60 (Fragment). | | |
| GN Cpn60. | | |
| SQ STREPTOCOCCUS VESTIBULARIS. | | |
| OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; | | |
| OC Streptococcaceae; Streptococcus. | | |
| OX NCBI_TAXID=1343; | | |
| RP [1] SEQUENCE FROM N.A. | | |
| RC STRAIN=ATCC43124; | | |
| RA Goh S.H., Hill J.E., Hemmingsen S.M.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | | |
| DR EMBL; AF25803; AAK48854.1; -. | | |
| DR Interpro; IPR002423; Cpn60/TCP-1. | | |
| DR Pfam; PF00118; cpn60_TCP1; 1. | | |
| KW Amp-binding; Chaperone. | | |
| FT NON-TER 1 1 | | |
| SQ SEQUENCE 184 AA; 19868 MW; DE048E8708C36177 CRC64; | | |
| Query Match Best Local Similarity 100.0%; Score 86; DB 2; Length 184; Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| OY 139 GKEATAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 198 | | |
| Db 49 GKEATAQVAVASSRSEKVEYISEAMERVGNDGVITIERSRGMETELLYEVGEGMDFRGYL 108 | | |
| DR 199 SQWYTDNEKMDArlenPFLITDKK 224 | | |
| Db 109 SQWYTDNEKMDArlenPFLITDKK 134 | | |

FT NON_TER 184 AA; 184 19864 MW; 8234ED8E164FC988 CRC64;
 SQ SEQUENCE 1478; Score 80; DB 2; Length 184;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.2e-73;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR EMBL; AF485791; AA196565.1; -;
 DR EMBL; AF485791; AA196570.1; -;
 DR EMBL; AF485792; AA196571.1; -;
 DR EMBL; AF485793; AA196572.1; -;
 DR EMBL; AF485792; AA196571.1; -;
 DR EMBL; AF485793; AA196572.1; -;
 DR NON_TER 159 159
 FT NON_TER 159 AA; 17391 MW; C5F4C7AB7753864C CRC64;
 SQ SEQUENCE 143; Score 78; DB 2; Length 159;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.2e-71;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR 133 IAPQPSGKELAQVAANSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQ 192
 DB 36 IAPQPSGKELAQVAANSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQ 95
 QY 193 FDGRGILSQMYTDNEKMY 210
 Db 96 FDGRGILSQMYTDNEKMY 113

RESULT 10
 ID 093TK7 PRELIMINARY; PRT; 184 AA.
 AC 093TK7;
 DR 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE Cpn60 (Fragment).
 GN CPN60.
 OS Streptococcus salivarius.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TAXID=1304;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC703;
 RA Goh S.H., Hill J.E., Hemmingsen S.M.;
 RT "Streptococcus species characterized by cpn60 sequence."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF52807; RAK48858.1; -;
 DR InterPro; IPR02423; Cpn60/TCP-1.
 DR Pfam; PF00118; Cpn60_TCP1; 1.
 KW ATP-binding, Chaperone.
 FT NON_TER 1
 FT NON_TER 184 184
 SQ SEQUENCE 184 AA; 19864 MW; 8234ED8E164FC988 CRC64;
 Query Match Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR 140 KERIAQAVAVSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQFDGRGYS 199
 DB 50 KERIAQAVAVSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQFDGRGYS 109

QY 200 QWVTDNEKMYTDNEKMY 219
 Db 110 QWVTDNEKMYTDNEKMY 129

RESULT 11
 ID Q8RJ02 PRELIMINARY; PRM; 159 AA.
 AC Q8RJ02;
 DR 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE kda chaperonin Cpn60 (Fragment).
 GN CPN60.
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TAXID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR STRAIN=ATCC 13813; ATCC 27956, 13821-4, AND 13824-5;
 RA McDonald W.L., Deighton M.A., Fry B.N.;
 RA McDonald W.L., Deighton M.A., Fry B.N.;

RESULT 12
 ID 093TK3 PRELIMINARY; PRT; 184 AA.
 AC 093TK3;
 DR 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE Cpn60 (Fragment).
 GN CPN60.
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TAXID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC1386;
 RA Goh S.H., Hill J.E., Hemmingsen S.M.;
 RT "Streptococcus species characterized by cpn60 sequence."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF52801; RAK48662.1; -;
 DR InterPro; IPR02423; Cpn60/TCP-1.
 DR Pfam; PF00118; Cpn60_TCP1; 1.
 KW ATP-binding, Chaperone.
 FT NON_TER 1
 FT NON_TER 184 184
 SQ SEQUENCE 184 AA; 20012 MW; D420B4EB24EBDFB CRC64;
 Query Match Best Local Similarity 14.3%; Score 78; DB 2; Length 184;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQPVSGKELAQVAANSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQ 192
 Db 43 IAQPVSGKELAQVAANSSRSEKVGELYSEAMERVGNDGVITIERSGRGMETELEVEMQ 102
 QY 193 FDGRGILSQMYTDNEKMY 210
 Db 103 FDGRGILSQMYTDNEKMY 120

RESULT 13
 ID Q9AME7 PRELIMINARY; PRT; 540 AA.
 AC Q9AME7;
 DR 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DR 60 kda chaperonin (protein Cpn60) (GroEL protein).
 OS Streptococcus agalactiae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OC NCBI_TaxID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jwo-Farm C.;
 RT "Cloning, sequencing, and characterization of 60 kDa chaperonin gene
 submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases."
 RL -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CONDITIONS (BY SIMILARITY).
 CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 7 SUBUNITS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL_AF322222; ARK12936; 1; -.
 DR HSSP; P06119; IGRU.
 DR InterPro; IPR001844; Chaperonin_Cpn60.
 DR Pfam; PF00118; Cpn60_TCP1; 1.
 DR PRINTS; PR00298; CHAPERONINO.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
 KW ATP-binding; Chaperone.
 SQ SEQUENCE 540 AA; 57287 MW; F392085FCF919BD1 CRC64;

Query Match 14.3%; Score 78; DB 2; Length 540;
 Best Local Similarity 100.0%; Pred. No. 3.7e-71; Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 IAQPVSGKEIAQAVAVSVRSRSEKVGEYISEAMERVNGDVITIERSMETELEVVEGMQ 192
 Db 133 IAQPVSGKEIAQAVAVSVRSRSEKVGEYISEAMERVNGDVITIERSMETELEVVEGMQ 192

Qy 193 FDGRGYSQWVTDNEKY 210
 Db 193 FDGRGYSQWVTDNEKY 210

RESULT 14

ID 069135 PRELIMINARY; PRT; 184 AA.
 AC 069135; DR 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-MAR-2002 (TREMBREL 07, last sequence update)
 DE 60 kDa chaperonin (Fragment),
 GN CPN60.
 OS Streptococcus iniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OC NCBI_TaxID=1346;
 RN [1]
 RP SEQUENCE FROM N.A.

RA SPRINT-ATCC29178;
 RX MEDLINE-#8313012; PubMed-#650992;
 RA Goh S.H., Drledger D., Gillett S., Low D.E., Hemmingsen S.M., Amos M., Chan D., Lovgren M., Willey B.M., Shaw C., Smith J.A.;
 RT Streptococcus iniae, a human and animal pathogen: specific identification by the chaperonin 60 gene identification method.;
 RL J. Clin. Microbiol. 35:2164-2166(1998).
 DR EMBL_AF06076; ARC16661.1; -.
 DR HSSP; P45746; ISRV.
 DR InterPro; IPR002423; Cpn60_TCP1.
 DR Pfam; PF00118; Cpn60_TCP1; 1.
 DR AMP-binding; Chaperone.
 FT NON_TER 1
 FT NON_TER 184 184 AA; 20009 MW; CE577F5CBA07B374 CRC64;

Query Match 13.8%; Score 75; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.7e-68;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

QX4R5 PRELIMINARY; PRT; 540 AA.
 AC 09X4R5
 CC 01-NOV-1999 (TREMBREL 12, Created)
 DT 01-NOV-1999 (TREMBREL 12, Last sequence update)
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OC NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CF1200.
 RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;
 RT "grossI sequences in Streptococcus pneumoniae."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDJB databases.
 CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CONDITIONS (BY SIMILARITY).
 CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 7 SUBUNITS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL_AF11741; AAC34455; 1.
 DR HSSP; P06119; IGRU.
 DR InterPro; IPR001844; Chaperonin_Cpn60.
 DR PRINTS; PR00298; CHAPERONINO.
 DR Pfam; PF00118; Cpn60_TCP1; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
 DR PRINTS; PR00298; CHAPERONINO.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
 DR ATP-binding; Chaperone.
 SQ SEQUENCE 540 AA; 57213 MW; 4QDB489AF1C6332DA CRC64;

Query Match 12.8%; Score 70; DB 2; Length 540;
 Best Local Similarity 100.0%; Pred. No. 5.6e-63;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 NRPLIITADDYGEALPTLVNLKIRGTPPPVVAKAGFGDRRKAMLEIDAILGGVITE 301
 Db 242 NRPLIITADDYGEALPTLVNLKIRGTPPPVVAKAGFGDRRKAMLEIDAILGGVITE 301
 Qy 302 DLSGLELKDAT 311
 Db 302 DLGLELKDAT 311

Search completed: April 8, 2003, 14:37:27
 Job time : 103 secs